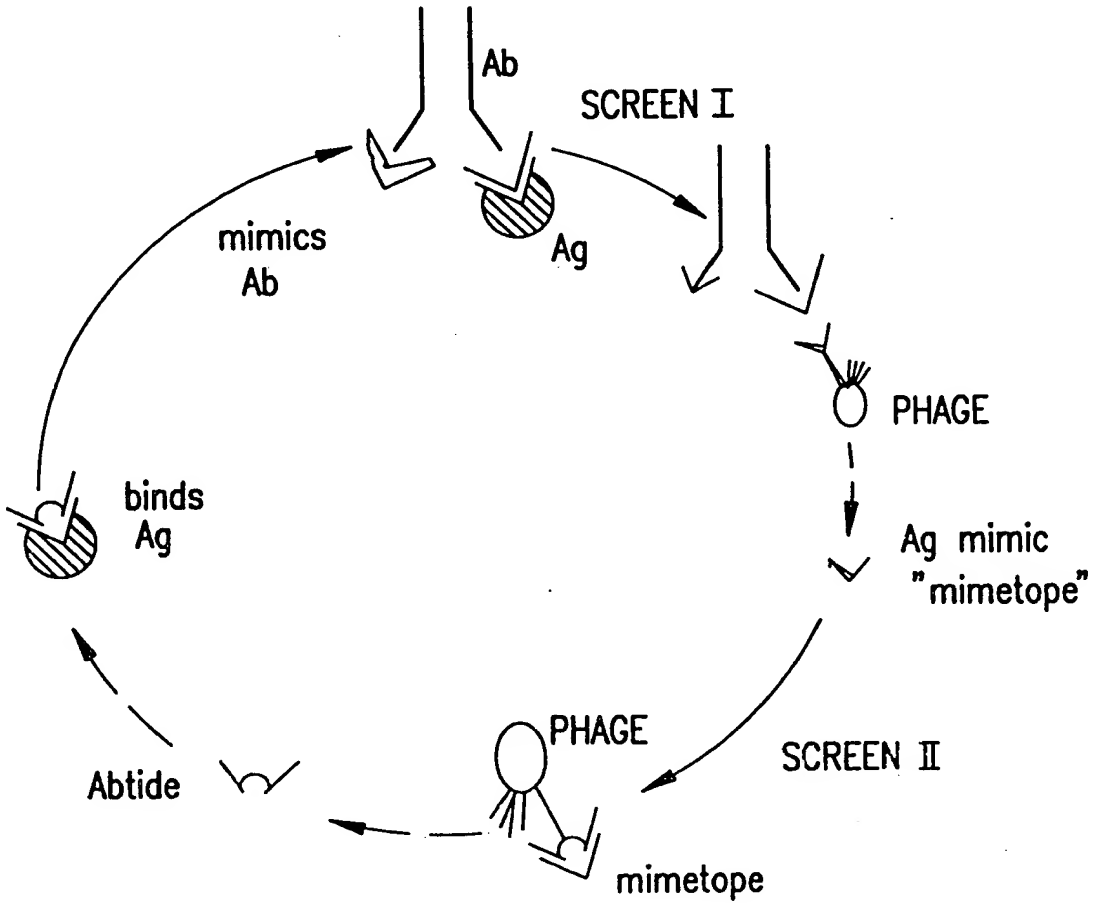

Ab
SCREEN I
Ag
mimics
Ab
PHAGE
Ag mimic
"mimetope"
SCREEN II
PHAGE
mimetope
Abtide
binds
Ag

FIG.1

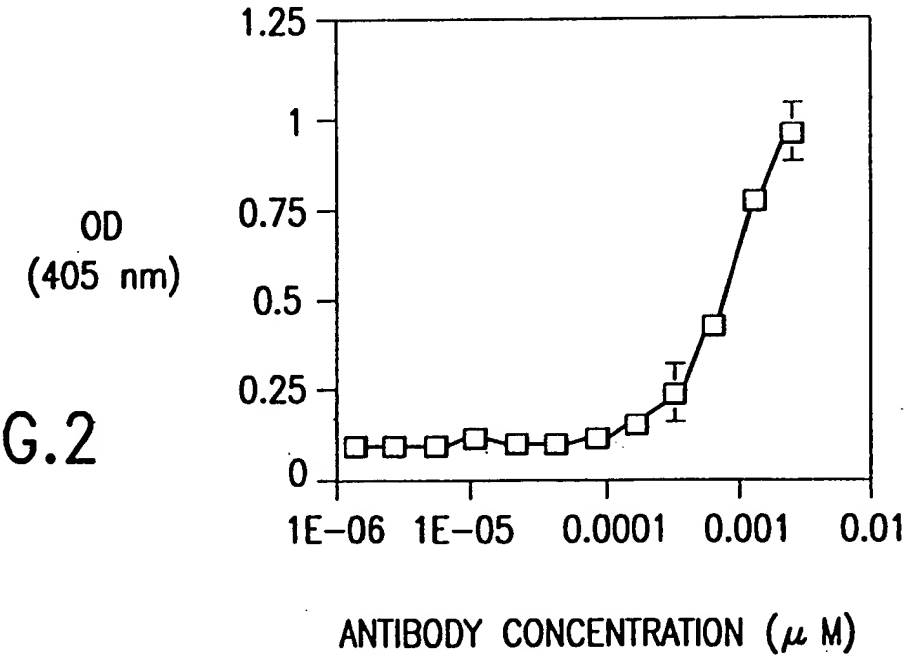

1.25
1
0.75
0.5
0.25
0
OD
(405 nm)
1E-06
1E-05
0.0001
0.001
0.01
ANTIBODY CONCENTRATION (μ M)

FIG.2

CLONE 14 GIINANDPLPFWFMS--PYTPGPAPIDINASRALVS-NESG
WQGTHFPYT LVSKNDSG
CDR3L CDR2L
(5/9 = 55.5 %) (7/8 = 87.5 %)

CLONE 17 DL-SRNLDFGRFLLYNA--YVPGFTPTFISLTAEHLSSPKG
LVSKN-DSG WQGTHF-P-YT
CDR2L CDR3L
(6/8 = 75 %) (6/9 = 66.6 %)

CLONE 15 CGRAYCL-SGNYNIFGALFPGVS--TPYADVGHDDAQSWRR
LVSKN-DS-G WQG-THFPYT
CDR2L CDR3L
(4/8 = 50 %) (6/9 = 66.6 %)

CLONE 13 RCSPIW-GIS-YPFGLLSSNPGVCHSSDAET-NIRNDILTT
WQG-THFPYT GSDN-K-SVL
CDR3L CDR2L(REV)
(6/9 = 66.6 %) (4/8 = 50 %)

CLONE 16 GHSNYCFVSTLGMPIVGFP-SINARGLIHYGGSDPR--LAA
WQGTHFPYT GSDNKSVL
CDR3L CDR2L(REV)
(3/9 = 33.3 %) (5/8 = 62.5 %)

FIG.3

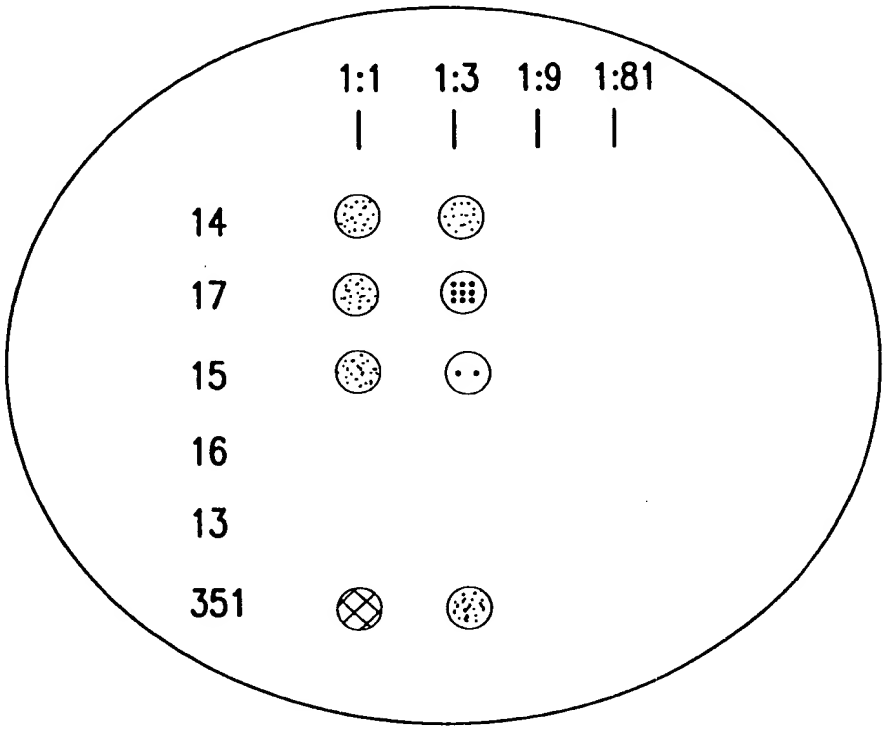

1:1
1:3
1:9
1:81
14
17
15
16
13
351

FIG.4

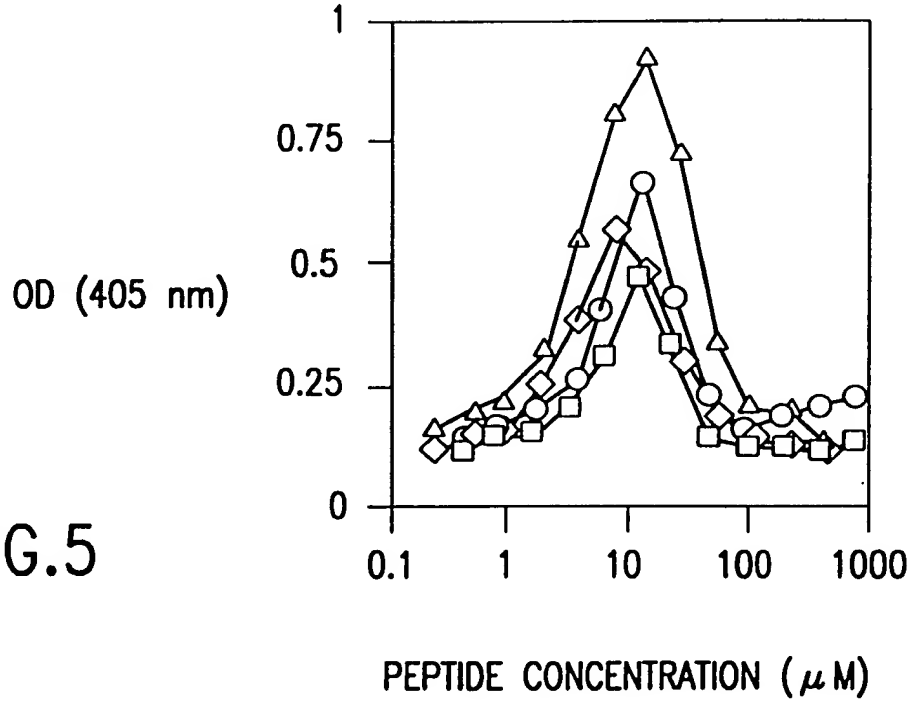

OD (405 nm)
1
0.75
0.5
0.25
0
0.1
1
10
100
1000
PEPTIDE CONCENTRATION (μM)

FIG.5

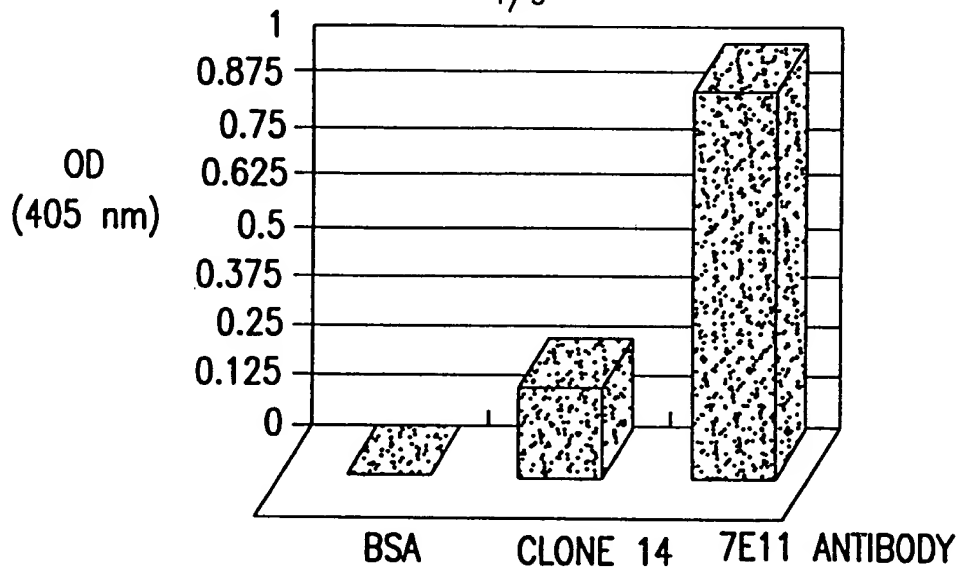

OD
(405 nm)
1
0.875
0.75
0.625
0.5
0.375
0.25
0.125
0
BSA
CLONE 14
7E11 ANTIBODY

FIG.6

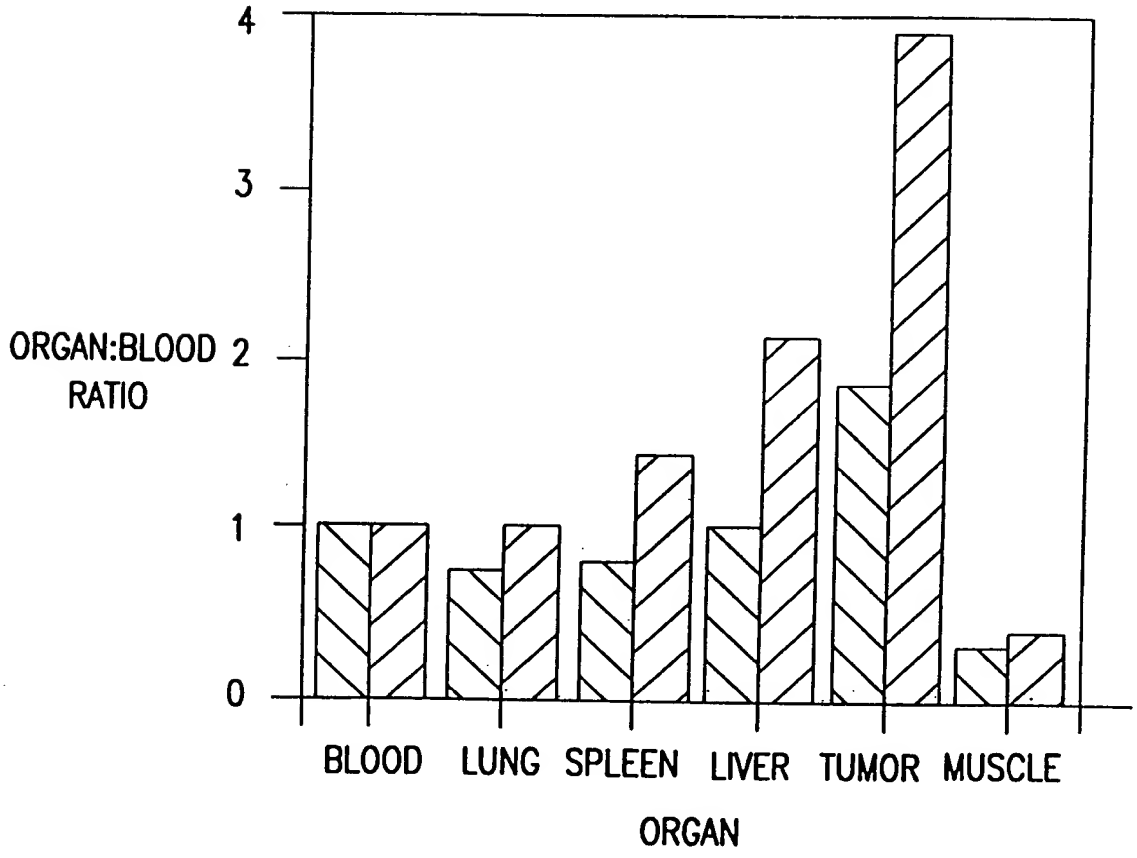

ORGAN:BLOOD
RATIO
4
3
2
1
0
BLOOD
LUNG
SPLEEN
LIVER
TUMOR
MUSCLE
ORGAN

FIG.7

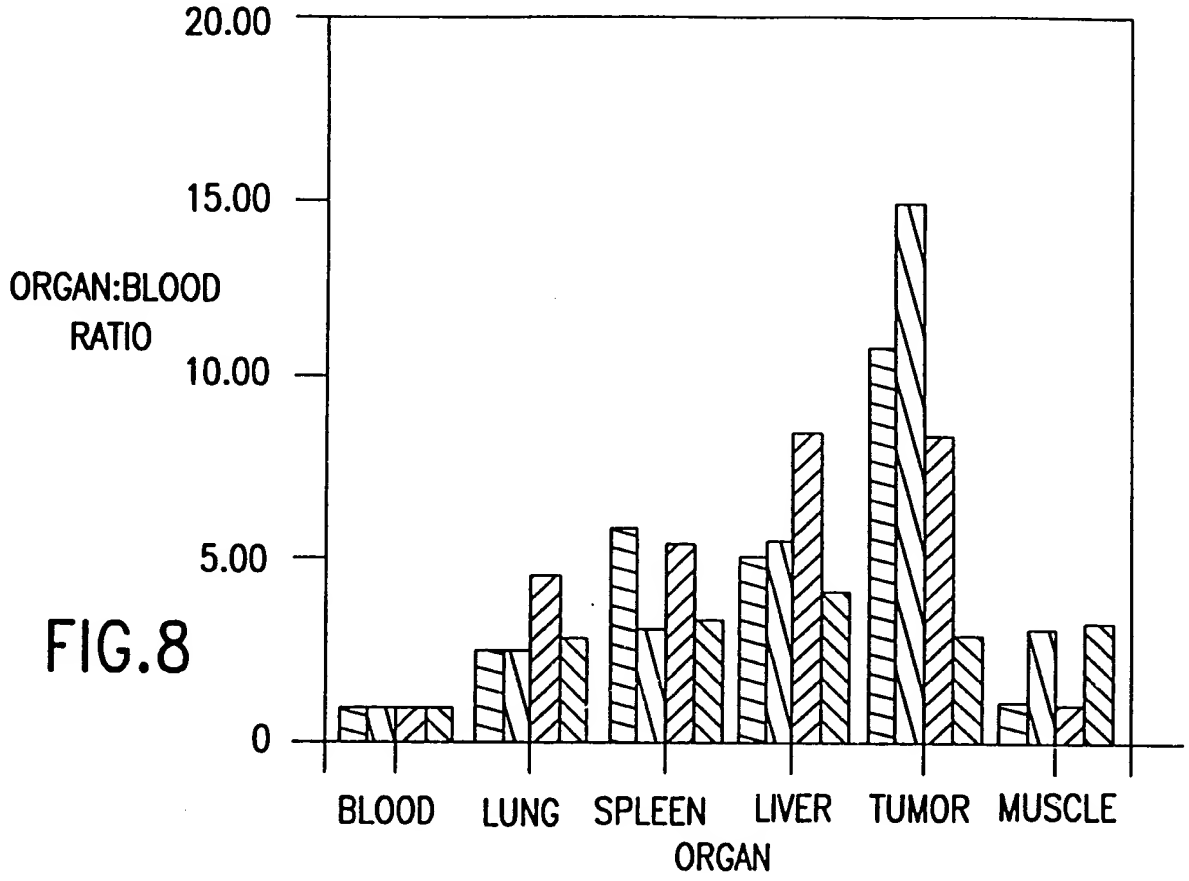

20.00
15.00
ORGAN:BLOOD
RATIO
10.00
5.00
0
BLOOD
LUNG
SPLEEN
LIVER
TUMOR
MUSCLE
ORGAN

FIG.8

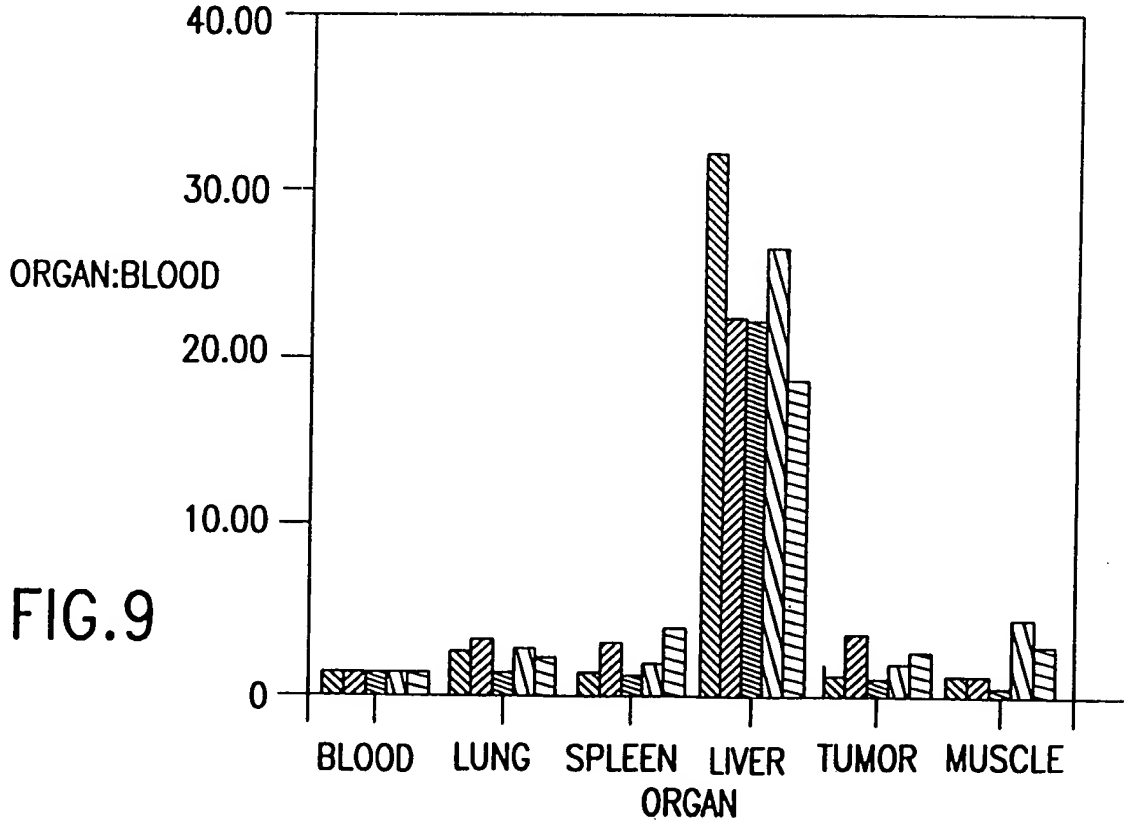

40.00
30.00
ORGAN:BLOOD
20.00
10.00
0
BLOOD
LUNG
SPLEEN
LIVER
TUMOR
MUSCLE
ORGAN

FIG.9

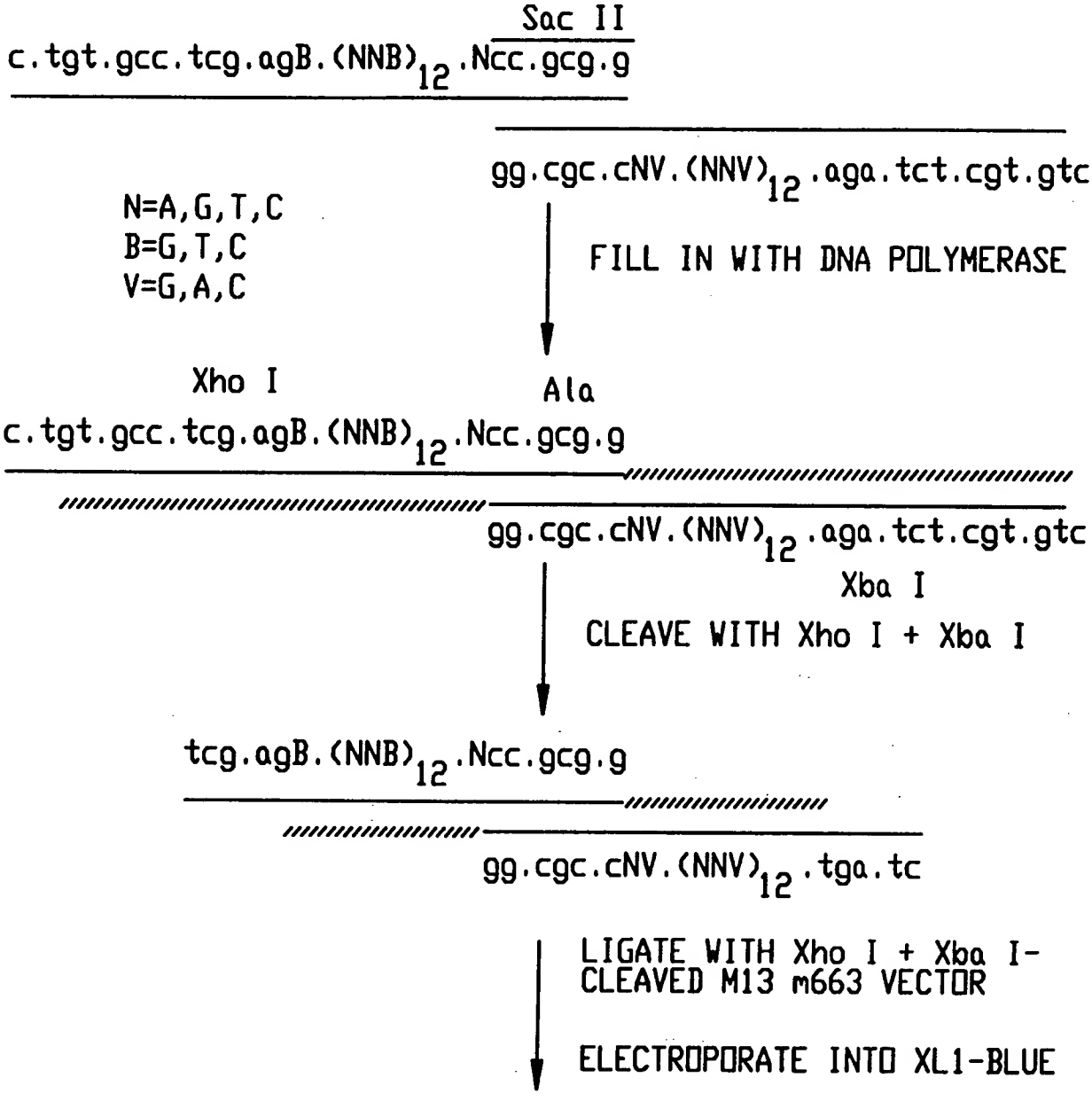
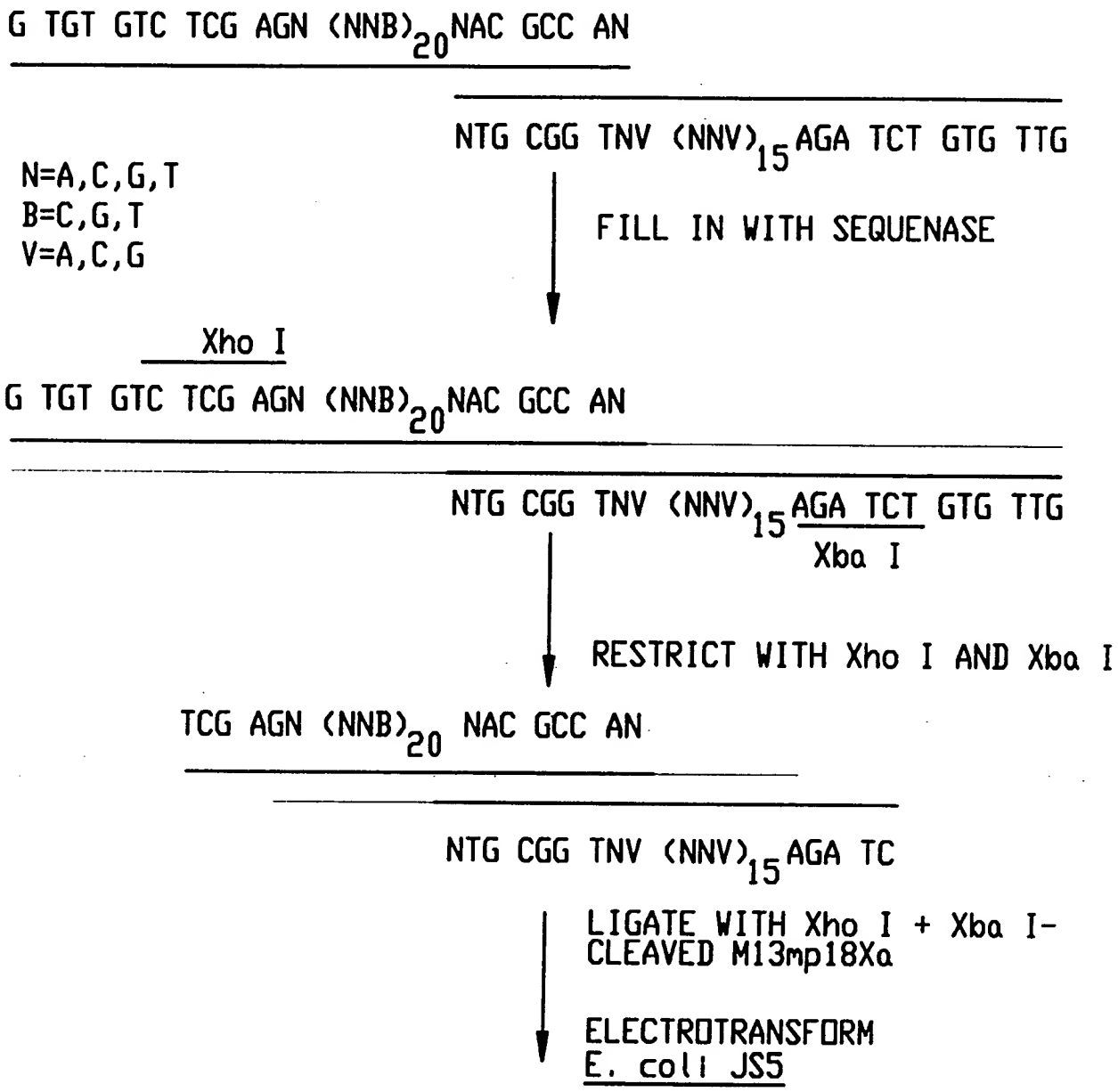

Sac II
c.tgt.gcc.tcg.agB.(NNB)12.Ncc.gcg.g
gg.cgc.cNV.(NNV)12.aga.tct.cgt.gtc
N=A,G,T,C
B=G,T,C
V=G,A,C
FILL IN WITH DNA POLYMERASE
Xho I
Ala
c.tgt.gcc.tcg.agB.(NNB)12.Ncc.gcg.g
gg.cgc.cNV.(NNV)12.aga.tct.cgt.gtc
Xba I
CLEAVE WITH Xho I + Xba I
tcg.agB.(NNB)12.Ncc.gcg.g
gg.cgc.cNV.(NNV)12.tga.tc
LIGATE WITH Xho I + Xba I-CLEAVED M13 m663 VECTOR
ELECTROPORATE INTO XL1-BLUE
LIBRARY OF pIII-RANDOM SEQUENCE FUSION PROTEINS
. . . S H S S (S/R) X12 π A ∂ X12 S R P S R T . . .
π=S,P,T OR A
∂=V,A,D,E, OR G
SIGNAL PEPTIDASE CLEAVAGE SITE

FIG.10



D38 GENETIC DIVERSITY LIBRARY DISPLAYED AS RANDOM N-TERMINAL pIII FUSIONS

. . H S S (S/R) X_{20} (Y/H/N/D) A (I/M/T/N/K/S/R) X_{15} S R

SIGNAL PEPTIDASE CLEAVAGE SITE

FIG.11

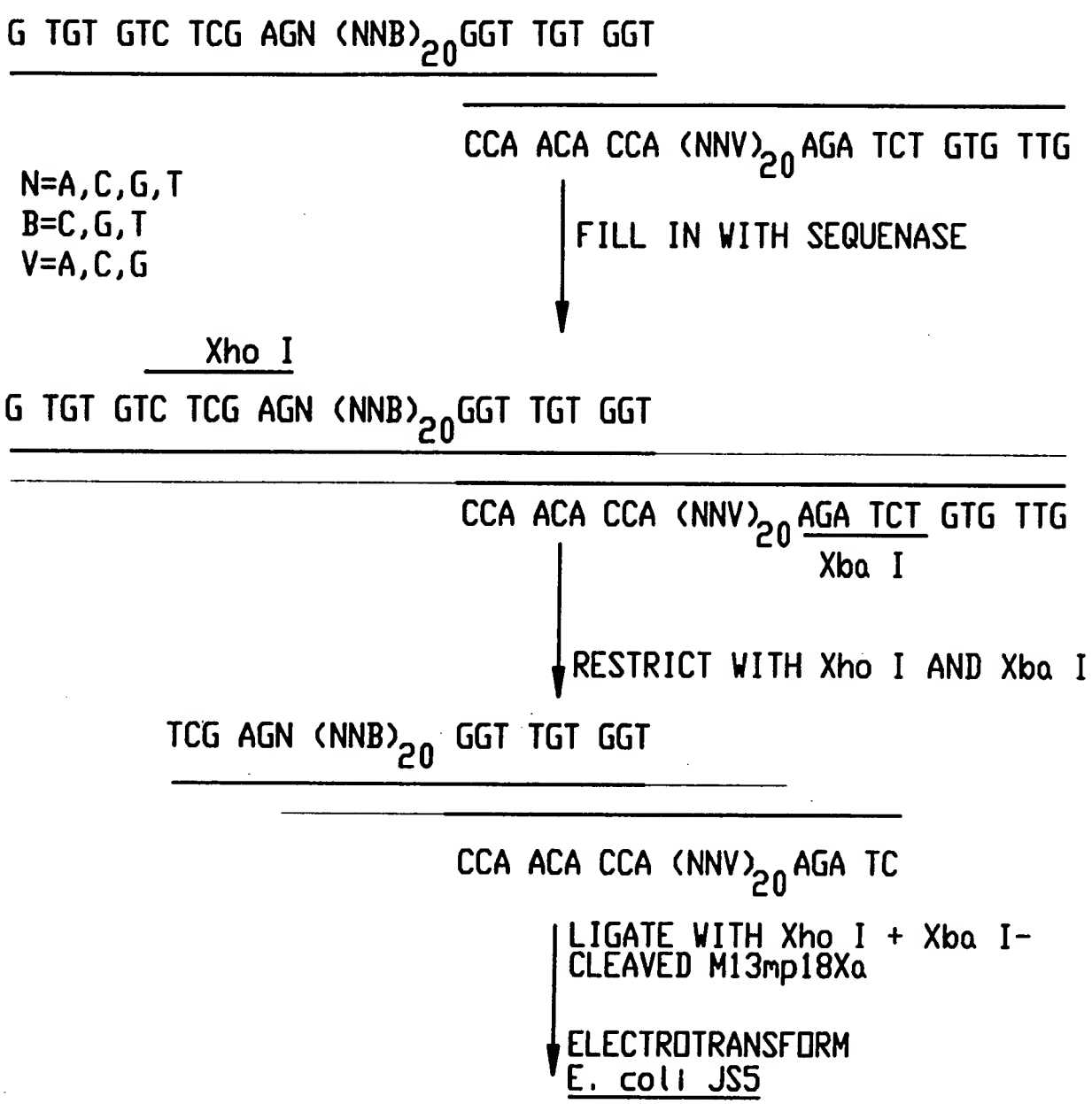

G TGT GTC TCG AGN (NNB)20GGT TGT GGT
CCA ACA CCA (NNV)20 AGA TCT GTG TTG
N=A,C,G,T
B=C,G,T
V=A,C,G
FILL IN WITH SEQUENASE
Xho I
G TGT GTC TCG AGN (NNB)20GGT TGT GGT
CCA ACA CCA (NNV)20 AGA TCT GTG TTG
Xba I
RESTRICT WITH Xho I AND Xba I
TCG AGN (NNB)20 GGT TGT GGT
CCA ACA CCA (NNV)20 AGA TC
LIGATE WITH Xho I + Xba I-CLEAVED M13mp18Xa
ELECTROTRANSFORM
E. coli JS5
DC43 GENETIC DIVERSITY LIBRARY DISPLAYED AS RANDOM N-TERMINAL pIII FUSIONS
. . H S S (S/R) X20 G C G X20 S R
SIGNAL PEPTIDASE CLEAVAGE SITE

FIG.12

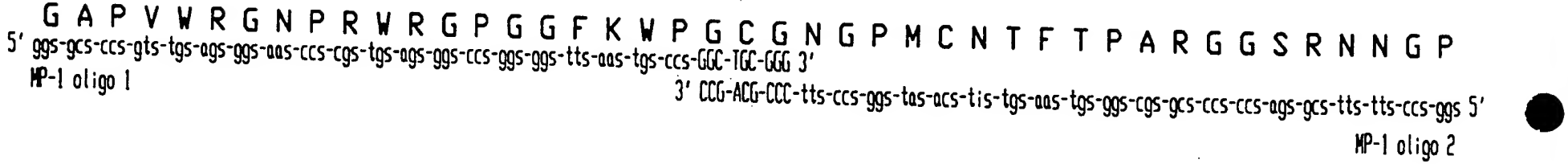

G A P V W R G N P R W R G P G G F K W P G C G N G P M C N T F T P A R G G S R N N G P
5' ggs-gcs-ccs-gts-tgs-ags-ggs-aas-ccs-cgs-tgs-ags-ggs-ccs-ggs-ggs-tts-aas-tgs-ccs-GGC-TGC-GGG 3'
MP-1 oligo 1
3' CCG-ACG-CCC-tts-ccs-ggs-tas-acs-tis-tgs-aas-tgs-ggs-cgs-gcs-ccs-ccs-ags-gcs-tts-tts-ccs-ggs 5'
MP-1 oligo 2

FIG.13